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RAW SEQUENCE LISTING DATE: 05/07/2002
PATENT APPLICATION: **US/10/075,987** TIME: 11:47:07

Input Set : **N:\Crf3\RULE60\10075987.raw**
Output Set: **N:\CRF3\05072002\J075987.raw**

<110> APPLICANT: Glucksmann, Maria A.
<120> TITLE OF INVENTION: 14273 Receptor, A Novel G-Protein Coupled Receptor
<130> FILE REFERENCE: 5800-4B, 035800/177086
<140> CURRENT APPLICATION NUMBER: 10/075,987
<141> CURRENT FILING DATE: 2002-02-13
<150> PRIOR APPLICATION NUMBER: US/09/261,599B
<151> PRIOR FILING DATE: 1999-02-26
<150> PRIOR APPLICATION NUMBER: 09/223,538
<151> PRIOR FILING DATE: 1998-12-30
<160> NUMBER OF SEQ ID NOS: 7
<170> SOFTWARE: PatentIn Ver. 2.1

ENTERED

<210> SEQ ID NO: 1
<211> LENGTH: 361
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 1

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Leu Glu Gln Ala Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys
            20                  25                  30
Gly Asp His Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val
        35                  40                  45
Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
    50                  55                  60
Val Ala Arg Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn
65                  70                  75                  80
Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu
                85                  90                  95
Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His
            100                 105                 110
Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr
        115                 120                 125
Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln
    130                 135                 140
Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala
145                 150                 155                 160
Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe
                165                 170                 175
Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser
            180                 185                 190
Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp
        195                 200                 205
Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
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210 215 220
Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
225 230 235 240
Leu Thr Val Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
245 250 255
Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
260 265 270
Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
275 280 285
Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
290 295 300
Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
305 310 315 320
Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys
325 330 335
Phe Trp Phe Pro Glu Lys Gly Ala Ile Leu Thr Asp Thr Ser Val Lys
340 345 350
Arg Asn Asp Leu Ser Ile Ile Ser Gly
355 360

<210> SEQ ID NO: 2
<211> LENGTH: 1743
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 2

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gcgggcagcg ggcgacgcgc ccttgcgcag cctggagcaa gccaaccgca cccgctttcc 120
cttcttctcc gacgtcaagg gcgaccaccg gctggtgctg gccgcggtgg agacaaccgt 180
gctggtgctc atctttgcag tgtcgctgct gggcaacgtg tgcgccctgg tgctggtggc 240
gcgccgacga cgccgcggcg cgactgcctg cctggtactc aacctcttct gcgcggacct 300
gctcttcatc agcgctatcc ctctggtgct ggccgtgcgc tggactgagg cctggctgct 360
gggccccgtt gcctgccacc tgctcttcta cgtgatgacc ctgagcggca gcgtcaccat 420
cctcacgctg gccgcggtca gcctggagcg catggtgtgc atcgtgcacc tgcagcgcgg 480
cgtgcggggt cctgggcggc gggcgcgggc agtgctgctg gcgctcatct ggggctattc 540
ggcggtcgcc gctctgcctc tctgcgtctt ctttcgagtc gtcccgcaac ggctccccgg 600
cgccgaccag gaaatttcga tttgcacact gatttggccc accattcctg gagagatctc 660
gtgggatgtc tcttttgtta ctttgaactt cttggtgcca ggactggtca ttgtgatcag 720
ttactccaaa attttacaga tcacaaaggc atcaaggaag aggctcacgg taagcctggc 780
ctactcggag agccaccaga tccgcgtgtc ccagcaggac ttccggctct tccgcaccct 840
cttcctcctc atggtctcct tcttcatcat gtggagcccc atcatcatca ccatcctcct 900
catcctgatc cagaacttca agcaagacct ggtcatctgg ccgtccctct tcttctgggt 960
ggtggccttc acatttgcta attcagccct aaaccccatc ctctacaaca tgacactgtg 1020
caggaatgag tggaagaaaa ttttttgctg cttctggttc ccagaaaagg gagccatttt 1080
aacagacaca tctgtcaaaa gaaatgactt gtcgattatt tctggctaat ttttctttat 1140
agccgagttt ctcacacctg gcgagctgtg gcatgctttt aaacagagtt catttccagt 1200
accctccatc agtgcaccct gctttaagaa aatgaaccta tgcaaataga catccacagc 1260
gtcggtaaat taaggggtga tcaccaagtt tcataatatt ttccctttat aaaaggattt 1320
gttggccagg tgcagtggtt catgcctgta atcccagcag tttgggaggc tgaggtgggt 1380
ggatcacctg aggtcaggag ttcgagacca acctgaccaa catggtgaga cccccgtctc 1440
tactaaaaat aaaaaaaaaa attagctggg agtggtggtg ggcacctgta atcctagcta 1500

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Input Set : N:\Crf3\RULE60\10075987.raw
Output Set: N:\CRF3\05072002\J075987.raw

cttgggaggc tgaaccagga gaatctcttg aacctgggag gcagaggttg cagtgagccg 1560
agatcgtgcc attgcactcc aaccagggca acaagagtga aactccatct taaaaaaaaa 1620
aaaaaaaaga tttgttatgg gttcctttta aatgtgaact tttttagtgt gtttgtaata 1680
tgatcaaatt taataaatat ttatttatga ctgttcagca aaaaaaaaaa aaaaaaaggg 1740
cgg 1743

<210> SEQ ID NO: 3
<211> LENGTH: 259
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: Description of Unknown Organism: Seven Transmembrane Segment Rhodopsin Superfamily

<400> SEQUENCE: 3

Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg
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Thr Pro Thr Asn Ile Phe Ile Leu Asn Leu Ala Val Ala Asp Leu Leu
20 25 30
Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly
35 40 45
Ser Glu Asp Trp Pro Phe Gly Ser Ala Leu Cys Lys Leu Val Thr Ala
50 55 60
Leu Asp Val Val Asn Met Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile
65 70 75 80
Ser Ile Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg
85 90 95
Arg Arg Thr Ser Pro Arg Arg Ala Lys Val Val Ile Leu Leu Val Trp
100 105 110
Val Leu Ala Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Val
115 120 125
Lys Thr Val Glu Glu Gly Asn Gly Thr Leu Asn Val Asn Val Thr Val
130 135 140
Cys Leu Ile Asp Phe Pro Glu Glu Ser Thr Ala Ser Val Ser Thr Trp
145 150 155 160
Leu Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu Pro
165 170 175
Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu Arg
180 185 190
Lys Ala Ala Lys Thr Leu Leu Val Val Val Val Val Phe Val Leu Cys
195 200 205
Trp Leu Pro Tyr Phe Ile Val Leu Leu Leu Asp Thr Leu Cys Leu Ser
210 215 220
Ile Ile Met Ser Ser Thr Cys Glu Leu Glu Arg Val Leu Pro Thr Ala
225 230 235 240
Leu Leu Val Thr Leu Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro
245 250 255
Ile Ile Tyr

<210> SEQ ID NO: 4
<211> LENGTH: 361
<212> TYPE: PRT

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Input Set : N:\Crf3\RULE60\10075987.raw
Output Set: N:\CRF3\05072002\J075987.raw

<213> ORGANISM: Murine ortholog
<400> SEQUENCE: 4

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Met Ser Pro Glu Cys Ala Gln Thr Thr Gly Pro Gly Pro Ser His Thr
 1               5                  10                  15
Leu Asp Gln Val Asn Arg Thr His Phe Pro Phe Phe Ser Asp Val Lys
            20                  25                  30
Gly Asp His Arg Leu Val Leu Ser Val Val Glu Thr Thr Val Leu Gly
        35                  40                  45
Leu Ile Phe Val Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
    50                  55                  60
Val Ala Arg Arg Arg Arg Arg Gly Ala Ser Ala Ser Leu Val Leu Asn
65                  70                  75                  80
Leu Phe Cys Ala Asp Leu Leu Phe Thr Ser Ala Ile Pro Leu Val Leu
                85                  90                  95
Val Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Val Cys His
            100                 105                 110
Leu Leu Phe Tyr Val Met Thr Met Ser Gly Ser Val Thr Ile Leu Thr
        115                 120                 125
Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val Arg Leu Arg
    130                 135                 140
Arg Gly Leu Ser Gly Pro Gly Arg Arg Thr Gln Ala Ala Leu Leu Ala
145                 150                 155                 160
Phe Ile Trp Gly Tyr Ser Ala Leu Ala Ala Leu Pro Leu Tyr Ile Leu
                165                 170                 175
Phe Arg Val Val Pro Gln Arg Leu Pro Gly Gly Asp Gln Glu Ile Pro
            180                 185                 190
Ile Cys Thr Leu Asp Trp Pro Asn Arg Ile Gly Glu Ile Ser Trp Asp
        195                 200                 205
Val Phe Phe Glu Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
    210                 215                 220
Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
225                 230                 235                 240
Leu Thr Leu Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
                245                 250                 255
Gln Gln Asp Tyr Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
            260                 265                 270
Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
        275                 280                 285
Ile Gln Asn Phe Arg Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
    290                 295                 300
Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
305                 310                 315                 320
Tyr Asn Met Ser Leu Phe Arg Asn Glu Trp Arg Lys Ile Phe Cys Cys
                325                 330                 335
Phe Phe Phe Pro Glu Lys Gly Ala Ile Phe Thr Asp Thr Ser Val Arg
            340                 345                 350
Arg Asn Asp Leu Ser Val Ile Ser Ser
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<210> SEQ ID NO: 5

RAW SEQUENCE LISTING DATE: 05/07/2002
PATENT APPLICATION: US/10/075,987 TIME: 11:47:07

Input Set : N:\Crf3\RULE60\10075987.raw
Output Set: N:\CRF3\05072002\J075987.raw

196 <211> LENGTH: 1560
197 <212> TYPE: DNA
198 <213> ORGANISM: Murine ortholog
199 <400> SEQUENCE: 5
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201 ttcacaccat cagtgaccac tccagacttg tccggcttta cccgaatctt cacagcggag 120
202 tcgatgaccc tcttgacagc cacgagcgcg cgcagctccg ccatcttccc ggacgcgtgg 180
203 gccgggcgcc cggcatgtcc cctgagtgtg cacagacgac gggccctggt ccctcgcaca 240
204 ccctggacca agtcaatcgc acccacttcc ctttcttctc ggatgtcaag ggcgaccacc 300
205 ggttggtgtt gagcgtcgtg gagaccaccg ttctgggact catctttgtc gtctcactgc 360
206 tgggcaacgt gtgtgctcta gtgctggtgg cgcgccgtcg gcgccgtggg gcgtcagcca 420
207 gcctggtgct caacctcttc tgcgcggatt tgctcttcac cagcgccatc cctctagtgc 480
208 tcgtcgtgcg ctggactgag gcctggctgt tggggcccgt cgtctgccac ctgctcttct 540
209 acgtgatgac aatgagcggc agcgtcacga tcctcacact ggccgcggtc agcctggagc 600
210 gcatggtgtg catcgtgcgc ctccggcgcg gcttgagcgg cccggggcgg cggactcagg 660
211 cggcactgct ggctttcata tggggttact cggcgctcgc cgcgctgccc ctctacatct 720
212 tgttccgcgt ggtcccgcag cgccttcccg gcggggacca ggaaattccg atttgcacat 780
213 tggattggcc caaccgcata ggagaaatct catgggatgt gtttttgag actttgaact 840
214 tcctggtgcc gggactggtc attgtgatca gttactccaa aattttacag atcacgaaag 900
215 catcgcggaa gaggcttacg ctgagcttgg catactctga gagccaccag atccgagtgt 960
216 cccaacaaga ctaccgactc ttccgcacgc tcttcctgct catggtttcc ttcttcatca 1020
217 tgtggagtcc catcatcatc accatcctcc tcatcttgat ccaaaacttc cggcaggacc 1080
218 tggtcatctg gccatccctt ttcttctggg tggtggcctt cacgtttgcc aactctgccc 1140
219 taaaccccat actgtacaac atgtcgctgt tcaggaacga atggaggaag atttttgct 1200
220 gcttcttttt tccagagaag ggagccattt ttacagatac gtctgtcagg cgaaatgact 1260
221 tgtctgttat ttccagctaa ctagcctctg gtgccaggtg aaccacggtg tgcatgtaaa 1320
222 gggagttaac ttcaaggaaa gcccaccagt gcgccctgct ttaaaaatac ccgacttcca 1380
223 acagcaggca tctacggagc cagcaaatta aggaatgatc gctcagtata aaaatatttt 1440
224 tccttaaaag aactttctat gggttccttt tgtgaacttt tttaagtgtg tttgtaatat 1500
225 gatctagtta ataaattttt atttataacg tgttcctaca aaaaaaaaaa aaaaaaaaaa 1560
227 <210> SEQ ID NO: 6
228 <211> LENGTH: 300
229 <212> TYPE: PRT
230 <213> ORGANISM: Homo sapiens
231 <220> FEATURE:
232 <223> OTHER INFORMATION: mature polypeptide of 14273
233 <400> SEQUENCE: 6
234 Leu Val Leu Val Ala Arg Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu
235 1 5 10 15
236 Val Leu Asn Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro
237 20 25 30
238 Leu Val Leu Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val
239 35 40 45
240 Ala Cys His Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr
241 50 55 60
242 Ile Leu Thr Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val
243 65 70 75 80
244 His Leu Gln Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val
245 85 90 95

VERIFICATION SUMMARY DATE: 05/07/2002
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